



SEQUENCE LISTING

Koontz, Jason
Sklar, Jeffrey

<120> FUSION OF JAZF1 AND JJAZ1 GENES IN
ENDOMETRIAL STROMAL TUMORS

<130> 05311-024001

<140> US 09/874,162

<141> 2001-06-04

<150> US 60/209,093

<151> 2000-06-02

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<211> 3010

<212> DNA

<213> Homo sapiens

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tgc gga ctc cac ttc ccc acc ctg gcc gac ctc atc gag cac atc gag 153
Cys Gly Leu His Phe Pro Thr Leu Ala Asp Leu Ile Glu His Ile Glu
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gac aac cac atc gat aca gat cca cgg gtt tta gaa aaa caa gaa tta 201
Asp Asn His Ile Asp Thr Asp Pro Arg Val Leu Glu Lys Gln Glu Leu
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Gln Gln Pro Thr Tyr Val Ala Leu Ser Tyr Ile Asn Arg Phe Met Thr
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A3

85

90

95

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ccc atc acc ccc tcc tct tca ttc cgc agc agc act ccg aca ggc agc 441
 Pro Ile Thr Pro Ser Ser Ser Phe Arg Ser Ser Thr Pro Thr Gly Ser
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gag tat gac gag gag gag gtg gac tat gag gag tcg gac agc gat gag 489
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35 40 45
Glu Leu Gln Gln Pro Thr Tyr Val Ala Leu Ser Tyr Ile Asn Arg Phe
50 55 60
Met Thr Asp Ala Ala Arg Arg Glu Gln Glu Ser Leu Lys Lys Lys Ile
65 70 75 80
Gln Pro Lys Leu Ser Leu Thr Leu Ser Ser Val Ser Arg Gly Asn
85 90 95
Val Ser Thr Pro Pro Arg His Ser Ser Gly Ser Leu Thr Pro Pro Val
100 105 110
Thr Pro Pro Ile Thr Pro Ser Ser Phe Arg Ser Ser Thr Pro Thr
115 120 125
Gly Ser Glu Tyr Asp Glu Glu Val Asp Tyr Glu Glu Ser Asp Ser
130 135 140
Asp Glu Ser Trp Thr Thr Glu Ser Ala Ile Ser Ser Glu Ala Ile Leu
145 150 155 160
Ser Ser Met Cys Met Asn Gly Gly Glu Glu Lys Pro Phe Ala Cys Pro
165 170 175
Val Pro Gly Cys Lys Lys Arg Tyr Lys Asn Val Asn Gly Ile Lys Tyr
180 185 190
His Ala Lys Asn Gly His Arg Thr Gln Ile Arg Val Arg Lys Pro Phe
195 200 205
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 Met Ala Pro Gln Lys His Gly Gly Gly Gly Gly Gly
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 Gly Ser Gly Pro Ser Ala Gly Ser Gly Gly Gly Gly Phe Gly Gly Ser
 15 20 25
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 Ala Ala Val Ala Ala Ala Thr Ala Ser Gly Gly Lys Ser Gly Gly Gly
 30 35 40
 agc tgt gga ggg ggt ggc agt tac tcg gcc tcc tcc tcc tcc tcc gcg 374
 Ser Cys Gly Gly Gly Gly Ser Tyr Ser Ala Ser Ser Ser Ser Ser Ala
 45 50 55 60
 gcg gca gcg gcg ggg gct gcg gtg tta ccg gtg aag aag ccg aaa atg 422
 Ala Ala Ala Ala Gly Ala Ala Val Leu Pro Val Lys Lys Pro Lys Met
 65 70 75

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 80 85 90

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 95 100 105

ata ttt ttg cac aga act ctt act tac atg tct cat cga aac tcc aga 566
 Ile Phe Leu His Arg Thr Leu Thr Tyr Met Ser His Arg Asn Ser Arg
 110 115 120

aca aac atc aaa agg aaa aca ttt aaa gtt gat gat atg tta tca aaa 614
 Thr Asn Ile Lys Arg Lys Thr Phe Lys Val Asp Asp Met Leu Ser Lys
 125 130 135 140

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 145 150 155

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 Leu Gln Leu Thr Phe Thr Gly Phe Phe His Lys Asn Asp Lys Pro Ser
 160 165 170

cca aac tca gaa aat gaa caa aat tct gtt acc ctg gaa gtc ctg ctt 758
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 190 195 200

caa gtt ccc aca ggt aaa aag cag gtg cct ttg att cct gac ctc aat 854
 Gln Val Pro Thr Gly Lys Lys Gln Val Pro Leu Ile Pro Asp Leu Asn
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 225 230 235

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 Phe Glu Pro Ser Asn Ser His Met Val Lys Ser Tyr Ser Leu Leu Phe
 240 245 250

aga gtg act cgt cca gga aga aga gag ttt aat gga atg att aat gga 998
 Arg Val Thr Arg Pro Gly Arg Arg Glu Phe Asn Gly Met Ile Asn Gly
 255 260 265

gaa acc aat gaa aat att gat gtc aat gaa gag ctt cca gcc aga aga 1046
 Glu Thr Asn Glu Asn Ile Asp Val Asn Glu Glu Leu Pro Ala Arg Arg
 270 275 280

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 Lys Arg Asn Arg Glu Asp Gly Glu Lys Thr Phe Val Ala Gln Met Thr
 285 290 295 300

gta ttt gat aaa aac agg cgc tta cag ctt tta gat ggg gaa tat gaa 1142
 Val Phe Asp Lys Asn Arg Arg Leu Gln Leu Leu Asp Gly Glu Tyr Glu
 305 310 315

gta gcc atg cag gaa atg gaa gaa tgt cca ata agc aag aaa aga gca 1190
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 320 325 330

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 Thr Trp Glu Thr Ile Leu Asp Gly Lys Arg Leu Pro Pro Phe Glu Thr
 335 340 345

ttt tct cag gga cct acg ttg cag ttc act ctt cgt tgg aca gga gag 1286
 Phe Ser Gln Gly Pro Thr Leu Gln Phe Thr Leu Arg Trp Thr Gly Glu
 350 355 360

acc aat gat aaa tct acg gct cct att gcc aaa cct ctt gcc act aga 1334
 Thr Asn Asp Lys Ser Thr Ala Pro Ile Ala Lys Pro Leu Ala Thr Arg
 365 370 375 380

aat tca gag agt ctc cat cag gaa aac aag cct ggt tca gtt aaa cct 1382
 Asn Ser Glu Ser Leu His Gln Glu Asn Lys Pro Gly Ser Val Lys Pro
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 Phe Tyr Gln Phe Leu Tyr Asn Asn Asn Thr Arg Gln Gln Thr Glu Ala
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 Arg Asp Asp Leu His Cys Pro Trp Cys Thr Leu Asn Cys Arg Lys Leu
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 Tyr Ser Leu Leu Lys His Leu Lys Leu Cys His Ser Arg Phe Ile Phe
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 Asn Tyr Val Tyr His Pro Lys Gly Ala Arg Ile Asp Val Ser Ile Asn
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 495 500 505

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A3

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575 580 585	
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A3

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 Gly Gly Ser Tyr Ser Ala Ser Ser Ser Ser Ser Ala Ala Ala Ala Ala
 50 55 60
 Gly Ala Ala Val Leu Pro Val Lys Lys Pro Lys Met Glu His Val Gln
 65 70 75 80
 Ala Asp His Glu Leu Phe Leu Gln Ala Phe Glu Lys Pro Thr Gln Ile
 85 90 95
 Tyr Arg Phe Leu Arg Thr Arg Asn Leu Ile Ala Pro Ile Phe Leu His
 100 105 110
 Arg Thr Leu Thr Tyr Met Ser His Arg Asn Ser Arg Thr Asn Ile Lys
 115 120 125
 Arg Lys Thr Phe Lys Val Asp Asp Met Leu Ser Lys Val Glu Lys Met
 130 135 140

Lys Gly Glu Gln Glu Ser His Ser Leu Ser Ala His Leu Gln Leu Thr
 145 150 155 160
 Phe Thr Gly Phe Phe His Lys Asn Asp Lys Pro Ser Pro Asn Ser Glu
 165 170 175
 Asn Glu Gln Asn Ser Val Thr Leu Glu Val Leu Leu Val Lys Val Cys
 180 185 190
 His Lys Lys Arg Lys Asp Val Ser Cys Pro Ile Arg Gln Val Pro Thr
 195 200 205
 Gly Lys Lys Gln Val Pro Leu Ile Pro Asp Leu Asn Gln Thr Lys Pro
 210 215 220
 Gly Asn Phe Pro Ser Leu Ala Val Ser Ser Asn Glu Phe Glu Pro Ser
 225 230 235 240
 Asn Ser His Met Val Lys Ser Tyr Ser Leu Leu Phe Arg Val Thr Arg
 245 250 255
 Pro Gly Arg Arg Glu Phe Asn Gly Met Ile Asn Gly Glu Thr Asn Glu
 260 265 270
 Asn Ile Asp Val Asn Glu Glu Leu Pro Ala Arg Arg Lys Arg Asn Arg
 275 280 285
 Glu Asp Gly Glu Lys Thr Phe Val Ala Gln Met Thr Val Phe Asp Lys
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 Arg Glu Lys Thr Ile Thr Gln Ile Glu Glu Phe Ser Asp Val Asn Glu

A3

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625	630	635
Glu Asn Tyr Gly Gln Lys Ile Ile Lys Lys Asn Leu Cys Arg Asn Phe		
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Met Leu His Leu Val Ser Met His Asp Phe Asn Leu Ile Ser Ile Met		
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Ser Ile Asp Lys Ala Val Thr Lys Leu Arg Glu Met Gln Gln Lys Leu		
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690	695	700
Gln Asn Gly Thr Ala Asn Gly Phe Ser Glu Ile Asn Ser Lys Glu Lys		
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gtcagcatgc atgactttta tcttattagc ataatgtcaa tagataaagc tgttaccaag 2040
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                                     Met Thr
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A3

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Gly Ile Ala Ala Ala Ser Phe Phe Ser Asn Thr Cys Arg Phe Gly Gly
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tgc gga ctc cac ttc ccc acc ctg gcc gac ctc atc gag cac atc gag 153
Cys Gly Leu His Phe Pro Thr Leu Ala Asp Leu Ile Glu His Ile Glu
      20                      25                      30

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gac aac cac atc gat aca gat cca cgg gtt tta gaa aaa caa gaa tta 201
Asp Asn His Ile Asp Thr Asp Pro Arg Val Leu Glu Lys Gln Glu Leu
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cag cag cca acc tat gtt gcc ctg agt tac ata aat aga ttc atg aca 249
Gln Gln Pro Thr Tyr Val Ala Leu Ser Tyr Ile Asn Arg Phe Met Thr
      55                      60                      65

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gat gct gcc cgc cga gag cag gag tcc cta aag aag aag att cag ccg 297
Asp Ala Ala Arg Arg Glu Gln Glu Ser Leu Lys Lys Lys Ile Gln Pro
      70                      75                      80

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aag ctc tcg ctg act ctg tcc agc tca gtg tct cga ggg aat gtg tcc 345
Lys Leu Ser Leu Thr Leu Ser Ser Val Ser Arg Gly Asn Val Ser
      85                      90                      95

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act ccc cca cgc cac agc agt gga agc ctt act ccc ccc gtg acc cca 393
Thr Pro Pro Arg His Ser Ser Gly Ser Leu Thr Pro Pro Val Thr Pro
      100                      105                      110

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ccc atc acc ccc tcc tct tca ttc cgc agc agc act ccg aca gag cca 441
Pro Ile Thr Pro Ser Ser Ser Phe Arg Ser Ser Thr Pro Thr Glu Pro
      115                      120                      125                      130

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aca cag atc tat aga ttt ctt cga act cgg aat ctc ata gca cca ata 489
Thr Gln Ile Tyr Arg Phe Leu Arg Thr Arg Asn Leu Ile Ala Pro Ile
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 Phe Leu His Arg Thr Leu Thr Tyr Met Ser His Arg Asn Ser Arg Thr
 150 155 160

aac atc aaa agg aaa aca ttt aaa gtt gat gat atg tta tca aaa gta 585
 Asn Ile Lys Arg Lys Thr Phe Lys Val Asp Asp Met Leu Ser Lys Val
 165 170 175

gag aaa atg aaa gga gag caa gaa tct cat agc ttg tca gct cat ttg 633
 Glu Lys Met Lys Gly Glu Gln Glu Ser His Ser Leu Ser Ala His Leu
 180 185 190

cag ctt acg ttt act ggt ttc ttc cac aaa aat gat aag cca tca cca 681
 Gln Leu Thr Phe Thr Gly Phe Phe His Lys Asn Asp Lys Pro Ser Pro
 195 200 205 210

aac tca gaa aat gaa caa aat tct gtt acc ctg gaa gtc ctg ctt gtg 729
 Asn Ser Glu Asn Glu Gln Asn Ser Val Thr Leu Glu Val Leu Leu Val
 215 220 225

aaa gtt tgc cac aaa aaa aga aag gat gta agt tgt cca ata agg caa 777
 Lys Val Cys His Lys Lys Arg Lys Asp Val Ser Cys Pro Ile Arg Gln
 230 235 240

gtt ccc aca ggt aaa aag cag gtg cct ttg att cct gac ctc aat caa 825
 Val Pro Thr Gly Lys Lys Gln Val Pro Leu Ile Pro Asp Leu Asn Gln
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aca aaa ccc gga aat ttc ccg tcc ctt gca gtt tcc agt aat gaa ttt 873
 Thr Lys Pro Gly Asn Phe Pro Ser Leu Ala Val Ser Ser Asn Glu Phe
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gaa cct agt aac agc cat atg gtg aag tct tac tcg ttg cta ttt aga 921
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 Val Thr Arg Pro Gly Arg Arg Glu Phe Asn Gly Met Ile Asn Gly Glu
 295 300 305

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 Thr Asn Glu Asn Ile Asp Val Asn Glu Glu Leu Pro Ala Arg Arg Lys
 310 315 320

cga aat cgt gag gat ggg gaa aag aca ttt gtt gca caa atg aca gta 1065
 Arg Asn Arg Glu Asp Gly Glu Lys Thr Phe Val Ala Gln Met Thr Val
 325 330 335

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 Phe Asp Lys Asn Arg Arg Leu Gln Leu Leu Asp Gly Glu Tyr Glu Val
 340 345 350

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A3

Trp Glu Thr Ile Leu Asp Gly Lys Arg Leu Pro Pro Phe Glu Thr Phe
 375 380 385
 tct cag gga cct acg ttg cag ttc act ctt cgt tgg aca gga gag acc 1257
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 aat gat aaa tct acg gct cct att gcc aaa cct ctt gcc act aga aat 1305
 Asn Asp Lys Ser Thr Ala Pro Ile Ala Lys Pro Leu Ala Thr Arg Asn
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 Tyr Gln Phe Leu Tyr Asn Asn Asn Thr Arg Gln Gln Thr Glu Ala Arg
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 Tyr Val Tyr His Pro Lys Gly Ala Arg Ile Asp Val Ser Ile Asn Glu
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 Cys Tyr Asp Gly Ser Tyr Ala Gly Asn Pro Gln Asp Ile His Arg Gln
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 Thr His Ile Leu Val Cys Arg Pro Lys Arg Thr Lys Ala Ser Met Ser
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 580 585 590
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 Ser Ser Gly His Asn Arg Leu Tyr Phe His Ser Asp Thr Cys Leu Pro

A3

595	600	605	610	
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Leu Arg Pro Gln Glu Met Glu Val Asp Ser Glu Asp Glu Lys Asp Pro				
	615	620	625	
gaa tgg cta aga gaa aaa acc att aca caa att gaa gag ttt tct gat				1977
Glu Trp Leu Arg Glu Lys Thr Ile Thr Gln Ile Glu Glu Phe Ser Asp				
	630	635	640	
gtt aat gaa gga gag aaa gaa gtg atg aaa ctc tgg aat ctc cat gtc				2025
Val Asn Glu Gly Glu Lys Glu Val Met Lys Leu Trp Asn Leu His Val				
	645	650	655	
atg aag cat ggg ttt att gct gac aat caa atg aat cat gcc tgt atg				2073
Met Lys His Gly Phe Ile Ala Asp Asn Gln Met Asn His Ala Cys Met				
	660	665	670	
ctg ttt gta gaa aat tat gga cag aaa ata att aag aag aat tta tgt				2121
Leu Phe Val Glu Asn Tyr Gly Gln Lys Ile Ile Lys Lys Asn Leu Cys				
	675	680	685	690
cga aac ttc atg ctt cat cta gtc agc atg cat gac ttt aat ctt att				2169
Arg Asn Phe Met Leu His Leu Val Ser Met His Asp Phe Asn Leu Ile				
	695	700	705	
agc ata atg tca ata gat aaa gct gtt acc aag ctc cgt gaa atg cag				2217
Ser Ile Met Ser Ile Asp Lys Ala Val Thr Lys Leu Arg Glu Met Gln				
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caa aaa tta gaa aag ggg gaa tct gct tcc cct gca aac gaa gaa ata				2265
Gln Lys Leu Glu Lys Gly Glu Ser Ala Ser Pro Ala Asn Glu Glu Ile				
	725	730	735	
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Thr Glu Glu Gln Asn Gly Thr Ala Asn Gly Phe Ser Glu Ile Asn Ser				
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aaa gag aaa gct ttg gaa aca gat agt gtc tca ggg gtt tca aaa cag				2361
Lys Glu Lys Ala Leu Glu Thr Asp Ser Val Ser Gly Val Ser Lys Gln				
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Ser Lys Lys Gln Lys Leu				
	775			
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tatgtttccaa acaggcactg ttagatgaag taaatgattt caacaaggat atttgatatca				2529
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A3

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Glu Leu Gln Gln Pro Thr Tyr Val Ala Leu Ser Tyr Ile Asn Arg Phe
50 55 60
Met Thr Asp Ala Ala Arg Arg Glu Gln Glu Ser Leu Lys Lys Lys Ile
65 70 75 80
Gln Pro Lys Leu Ser Leu Thr Leu Ser Ser Val Ser Arg Gly Asn
85 90 95
Val Ser Thr Pro Pro Arg His Ser Ser Gly Ser Leu Thr Pro Pro Val
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Thr Pro Pro Ile Thr Pro Ser Ser Phe Arg Ser Ser Thr Pro Thr
115 120 125
Glu Pro Thr Gln Ile Tyr Arg Phe Leu Arg Thr Arg Asn Leu Ile Ala
130 135 140
Pro Ile Phe Leu His Arg Thr Leu Thr Tyr Met Ser His Arg Asn Ser
145 150 155 160
Arg Thr Asn Ile Lys Arg Lys Thr Phe Lys Val Asp Asp Met Leu Ser
165 170 175
Lys Val Glu Lys Met Lys Gly Glu Gln Glu Ser His Ser Leu Ser Ala
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His Leu Gln Leu Thr Phe Thr Gly Phe Phe His Lys Asn Asp Lys Pro
195 200 205
Ser Pro Asn Ser Glu Asn Glu Gln Asn Ser Val Thr Leu Glu Val Leu

210 215 220
 Leu Val Lys Val Cys His Lys Lys Arg Lys Asp Val Ser Cys Pro Ile
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 275 280 285
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 325 330 335
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 Glu Val Ala Met Gln Glu Met Glu Glu Cys Pro Ile Ser Lys Lys Arg
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 Ala Thr Trp Glu Thr Ile Leu Asp Gly Lys Arg Leu Pro Pro Phe Glu
 370 375 380
 Thr Phe Ser Gln Gly Pro Thr Leu Gln Phe Thr Leu Arg Trp Thr Gly
 385 390 395 400
 Glu Thr Asn Asp Lys Ser Thr Ala Pro Ile Ala Lys Pro Leu Ala Thr
 405 410 415
 Arg Asn Ser Glu Ser Leu His Gln Glu Asn Lys Pro Gly Ser Val Lys
 420 425 430
 Pro Thr Gln Thr Ile Ala Val Lys Glu Ser Leu Thr Thr Asp Leu Gln
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 Thr Arg Lys Glu Lys Asp Thr Pro Asn Glu Asn Arg Gln Lys Leu Arg
 450 455 460
 Ile Phe Tyr Gln Phe Leu Tyr Asn Asn Asn Thr Arg Gln Gln Thr Glu
 465 470 475 480
 Ala Arg Asp Asp Leu His Cys Pro Trp Cys Thr Leu Asn Cys Arg Lys
 485 490 495
 Leu Tyr Ser Leu Leu Lys His Leu Lys Leu Cys His Ser Arg Phe Ile
 500 505 510
 Phe Asn Tyr Val Tyr His Pro Lys Gly Ala Arg Ile Asp Val Ser Ile
 515 520 525
 Asn Glu Cys Tyr Asp Gly Ser Tyr Ala Gly Asn Pro Gln Asp Ile His
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 Arg Gln Pro Gly Phe Ala Phe Ser Arg Asn Gly Pro Val Lys Arg Thr
 545 550 555 560
 Pro Ile Thr His Ile Leu Val Cys Arg Pro Lys Arg Thr Lys Ala Ser
 565 570 575
 Met Ser Glu Phe Leu Glu Ser Glu Asp Gly Glu Val Glu Gln Gln Arg
 580 585 590
 Thr Tyr Ser Ser Gly His Asn Arg Leu Tyr Phe His Ser Asp Thr Cys
 595 600 605
 Leu Pro Leu Arg Pro Gln Glu Met Glu Val Asp Ser Glu Asp Glu Lys
 610 615 620
 Asp Pro Glu Trp Leu Arg Glu Lys Thr Ile Thr Gln Ile Glu Glu Phe
 625 630 635 640
 Ser Asp Val Asn Glu Gly Glu Lys Glu Val Met Lys Leu Trp Asn Leu
 645 650 655
 His Val Met Lys His Gly Phe Ile Ala Asp Asn Gln Met Asn His Ala
 660 665 670

A3

Cys	Met	Leu	Phe	Val	Glu	Asn	Tyr	Gly	Gln	Lys	Ile	Ile	Lys	Lys	Asn
	675						680					685			
Leu	Cys	Arg	Asn	Phe	Met	Leu	His	Leu	Val	Ser	Met	His	Asp	Phe	Asn
	690						695				700				
Leu	Ile	Ser	Ile	Met	Ser	Ile	Asp	Lys	Ala	Val	Thr	Lys	Leu	Arg	Glu
705						710				715					720
Met	Gln	Gln	Lys	Leu	Glu	Lys	Gly	Glu	Ser	Ala	Ser	Pro	Ala	Asn	Glu
						725				730					735
Glu	Ile	Thr	Glu	Glu	Gln	Asn	Gly	Thr	Ala	Asn	Gly	Phe	Ser	Glu	Ile
						740				745					750
Asn	Ser	Lys	Glu	Lys	Ala	Leu	Glu	Thr	Asp	Ser	Val	Ser	Gly	Val	Ser
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Lys	Gln	Ser	Lys	Lys	Gln	Lys	Leu								
	770						775								

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 <212> DNA
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A3

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	tcattccgca	gcagcactcc	gacagagcca	acacagatct	atagatttct	tcgaactcgg	420
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gaacaaaatg ggacagcaaa tggatttagt gaaattaact caaaagagaa agctttggaa 2280
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<220>
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<220>
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<220>
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<400> 12
atcaccccct cctcttcatt 20

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<210> 13
<211> 20
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<220>
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<210> 14
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<220>
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26

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22

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<213> Artificial Sequence

<220>

<223> primer for PCR

<400> 17

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21

<210> 18

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> primer for PCR

<400> 18

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20

<210> 19

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<212> DNA

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A3

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